b.) Amendments to the Specification

Please insert the following new paragraph on page 1, line 5.

This application is a continuation of application No. 09/485,951 filed February 17, 2000 which in turn is the national phase of PCT application No. PCT/JP98/03670 filed August 19, 1998.

Please amend the paragraph at page 2, lines 14-22 to read as follows.

As the result of intensive studies, the present inventors have been successful in cloning of human cDNAs coding for galectin-9-like proteins, thereby completing the present invention. In other words, the present invention provides galectin-9-like proteins, namely proteins containing the amino acid sequences represented by ~~Sequence No. 1~~ SEQ ID NO:1 and ~~Sequence No. 2~~ SEQ ID NO:2. Moreover, the present invention provides cDNAs coding for the above-mentioned proteins and containing the base sequences represented by ~~Sequence No. 3 to Sequence No. 5~~ SEQ ID NO:3 to SEQ ID NO:5.

Please amend the paragraph starting at page 4, line 21 and ending at page 5, line 4, to read as follows.

The proteins of the present invention include peptide fragments (more than 5 amino acid residues) containing any partial amino acid sequence in the amino acid sequence represented by ~~Sequence No. 1~~ SEQ ID NO:1. These peptide fragments can be

utilized as antigens for preparation of antibodies. Hereupon, the proteins of the present invention are secreted in an extracellular manner. Since a portion capable of binding sugar chains exists in the amino acid sequence, proteins where sugar chains are added can be obtained by expression in appropriate animal cells. Accordingly, such proteins or peptides wherein sugar chains are added shall come within the scope of the present invention.

Please amend the paragraphs at page 6, lines 2-20 to read as follows.

The cDNAs of the present invention are characterized by containing the base sequence represented by ~~Sequence No. 3 or Sequence No. 4~~ SEQ ID NO:3 or SEQ ID NO:4. For example, that represented by ~~Sequence No. 5~~ SEQ ID NO:5 possesses a 1725-bp base sequence with a 1068-bp open reading frame. This open reading frame codes for a protein consisting of 355 amino acid residues. This protein possesses such a high 69.3% analogy to the mouse galectin-9-like isoform in the amino acid sequence level.

Hereupon, the same clones as the cDNAs of the present invention can be easily obtained by screening of the human cDNA libraries constructed from the human cells by the use of an oligonucleotide probe synthesized on the basis of the cDNA base sequence described in ~~Sequence No. 3~~ SEQ ID NO:3.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Accordingly, any cDNA that is subjected to insertion or deletion of one or plural nucleotides and/or substitution with other nucleotides in ~~Sequence No. 3 to~~

~~Sequence No. 5~~ SEQ ID NO:3 to SEQ ID NO:5 shall come within the scope of the present invention.

Please amend the paragraph starting at page 6, line 26 and ending at page 7, line 4 to read as follows.

The cDNAs of the present invention include cDNA fragments (more than 10 bp) containing any partial base sequence in the base sequence represented by ~~Sequence No. 3~~ SEQ ID NO:3. Also, DNA fragments consisting of a sense chain and an anti-sense chain shall come within this scope. These DNA fragments can be utilized as the probes for the gene diagnosis.

Please amend the paragraph starting at page 13, line 13 and ending at page 14, line 16 to read as follows.

Clone HP01461 was obtained as the result of a large-scale sequencing of cDNA clones selected from the cDNA library of human stomach cancer cells (described in W097/03190) . The present clone has a structure consisting of an 81-bp 5'-nontranslation region, a 1068-bp open reading frame, a 576-bp 3'-nontranslation region, and an 83-bp poly(A) tail (~~Sequence No. 5~~ SEQ ID NO:5) . The open reading frame codes for a protein consisting of 355 amino acid residues and the search of the protein data base using this sequence has revealed the presence of a high analogy to the amino acid sequences of human galectin-9 and mouse galectin-9 isoform. Table 2 shows the comparison of the amino acid sequence between the human galectin-like protein (HS) (SEQ ID NO:2) of the

present invention and the human galectin-9 (G9) (SEQ ID NO:7), while Table 3 shows the comparison of the amino acid sequence between the human galectin-like protein (HS) (SEQ ID NO:2) of the present invention and the mouse galectin-9 isoform (MM) SEQ ID NO:8. Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with the protein of the present invention, and an amino acid residue analogous to the protein of the present invention, respectively. Comparison of the protein of the present invention with human galectin-9 has revealed that there are differences at the following 6 sites. That is to say, they are lysine at position 88 (arginine in G), insertion of glycine at position 96, serine at position 135 (phenylalanine in G9), insertion of 32 amino acid residues from position 149 to position 180, proline at position 270 (leucine in G9), and glutamic acid at position 313 (glycine in G9) . Because comparison of the protein of the present invention with the mouse galectin-9 isoform has revealed that the protein of the present invention has a sequence that is longer only by 2 amino acid residues and a 69.3% analogy is shown in the entire region, the protein of the present invention is considered to be a homologue of the mouse galectin-9 isoform.

Please amend the paragraph starting at page 15, line 32, and ending at page 16, line 20 to read as follows.

Vector pHP01461 bearing the cDNA of the present invention was used for in vitro translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [^{35}S] methionine was added to label the expression product with a radioisotope. Each of the

reactions was carried out according to the protocols attached to the kit. Two micrograms of plasmid pHP01416 was reacted at 30°C for 90 minutes in a total 100 μl volume of the reaction solution containing 50 μl of T_NT rabbit reticulocyte lysate, 4 μl of a buffer solution (attached to kit), 2 μl of an amino acid mixture (methionine-free), 8 μl of [^{35}S] methionine (Amersham) (0.37 MBq/μl), 2 μl of T7RNA polymerase, and 80 U of RNasin. To 3 μl of the resulting reaction solution was added 2 μl of the SDS sampling buffer (125 mM Tris-hydrochloric acid buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0. 025% bromophenol blue, and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. Determination of the molecular weight of the translation product by carrying out the autoradiograph indicated that the cDNA of the present invention yielded the translation product with the molecular mass of about 40 kDa (Figure 2). This value is consistent with the molecular weight of 39,517 predicted for the putative protein from the base sequence represented by ~~Sequence No. 2~~ (SEQ ID NO:2), thereby indicating that this cDNA certainly codes for the protein represented by ~~Sequence No. 2~~ SEQ ID NO:2.

Please amend the paragraph at page 18, lines 5-15 to read as follows.

Two strands of an oligonucleotide primer PR1 (5'-CGCATATGGCCTTCAGCGGTTCCCAGGC-3') (SEQ ID NO:9) and PR2 (5' -AACGGCACCGTGGAGAAGGCAGGCTGAACA-3') (SEQ ID NO:10) were synthesized by using a DNA synthesizer (Applied Biosystems) according to the attached protocol. The

5'-tanslation region in the cDNA was amplified with the PCR kit (TAKARA SHUZO) using 1 ng of plasmid pHP01461 as well as 100 pmole each of primers PR1 and PR2. After phenol extraction and ethanol extraction, followed by digestion with 20 units of SacI and NdeI, the reaction product was subjected to 1.2% agarose electrophoresis to cut off an about 320-bp DNA fragment for purification.

Please amend the paragraph at page 19, lines 16-27 to read as follows.

Northern blot hybridization was carried out in order to examine the expression pattern in the human tissues. Filters where poly $(A)^+$ RNAs isolated from each of human tissues are blotted were purchased from Clontech. After digestion of plasmid pHP01049 with ApaLI and BstXI, followed by agarose-gel electrophoresis to isolate a cDNA fragment, labeling with [^{32}P]dCTP (Amersham) was carried out by using a random primer labeling kit (TAKARA SHUZO) . Furthermore, the inserted portion was subjected to the terminal ^{32}P-labeling with a synthetic oligonucleotide 5'-AACGGCACCGTGGAGAAGGCAGGCTGAGCA-3' (SEQ ID NO:11) using T4 polynucleotide kinase. The hybridization was carried out by using a solution attached to the blot paper according to the protocol.